REMARKS

THE AMENDMENTS

The specification has been amended to correct clear errors. At page 11, first paragraph, the method of using sodium metabisulphite is described. This chemical reagent does not introduce CpG dinucleotides as previously stated, but rather modifies them by converting unmethylated cytosine residues to uracil. This is supported within the same paragraph where the applicants teach that sodium metabisulphite "thereby convert[s] all unmethylated cytosine residues to uracil."

At page 12, second full paragraph, "unmethylated" NRE has been corrected to "methylated" NRE. The error is obvious from the context of the paragraph as originally presented:

> Subjects who have an unmethylated NRE can be kept under closer observation for early detection of relapse. This will maximize their chances for recovery. However, the expense of such close observation post-treatment is not necessary with subjects with ***un***methylated NRE.

These corrections to the specification do not add new matter.

The claims have been amended to clarify the intended meaning. The following recitations have been added which are supported in the specification:

RECITATION	SUPPORT IN SPECIFICATION
WT1 antisense regulatory region (ARR) and/or WT1 negative regulatory element (NRE)	Page 3, last paragraph, through page 4, third paragraph
And determining therefrom the presence or absence of Wilms' tumour and or prognosis of cancer in the subject based on the determined methylation state	Page 5, first full paragraph

RECITATION	SUPPORT IN SPECIFICATION
WT1 NRE comprising SEQ ID NO: 8 or 9	Pages 15 and 16
Nucleotide sequence comprising SEQ ID NO: 8 or 9	Pages 15 and 16

CLAIM OBJECTIONS

- Improper multiple dependencies: multiple dependencies have been removed from the claims. Consideration of all claims on the merits is therefore requested.
- Claim 22 has been cancelled, so the objection to it is now rendered moot.

CLAIM DEFINITENESS

The preamble of claim 7 has been amended to eliminate the confusing aspect of diagnosing a subject for whom a diagnosis has already been made.

Claims 7, 10, and 11 have been amended to recite a final process step which refers back to the preamble, as suggested by the examiner.

ENABLEMENT

The claims were rejected as too broad for the enablement provided. The PTO acknowledged that the specification did indeed enable certain subject matter, specifically testing specific nucleic acid sequences. Applicants have amended the claims to recite the specific nucleotide sequences ARR and NRE. It is respectfully submitted that these amendments render the claims commensurate in scope with the enablement provided by the specification.

WRITTEN DESCRIPTION

The claims were rejected as encompassing a genus of nucleic acid sequences which was not described by an adequate number of representative species. The claims have been amended to recite only ARR and/or NRE. It is respectfully submitted that these amendments put the claim in compliance with the written description requirement.

DUFFY (U.S. PATENT NO. 5,871,917)

Claims 7 and 21-23 stand rejected as anticipated by Duffy (U.S. Patent No. 5,871,917) under 35 U.S.C 102 (b). Claims 21-22 have been cancelled. This rejection is respectfully traversed with respect to claims 7 and 23.

Claim 7 has been amended to recite a method of diagnosis of Wilms' tumour or of prognosis of cancer by analysis of a nucleotide sequence or sequences comprising the WT1 antisense regulatory region (ARR) and/or WT1 negative regulatory element (NRE). Duffy does not teach methylation analysis of these specific genomic elements (ARR and NRE) nor their association with diagnosis of Wilms' Tumour or prognosis of cancer.

Claim 23 has been amended to recite a method for the diagnosis of Wilms' tumour comprising detection of the methylation state of a specific nucleotide sequence or sequences comprising ARR or NRE and concluding therefrom on the presence or absence of cancer wherein hypomethylation of the specific nucleotide sequence or sequences indicates the presence of cancer cells in the subject. Duffy does not teach that hypomethylation of nucleic acid sequence is present in Wilms' Tumour samples. For at least the above reasons, the present rejection should be withdrawn.

NELSON ET AL. (U.S. PATENT NO. 5,552,277).

Claims 21-23 also stand rejected under 35 U.S.C 102 (b), as anticipated by Nelson et al. (U.S. Patent No. 5,552,277). Claims 21 and 22 are cancelled. Applicant traverses the rejection with respect to claim 23.

Claim 23 has been amended to recite a method for the diagnosis of Wilms' tumour comprising detection of the methylation state of a specific nucleotide sequence or sequences and concluding therefrom on the presence or absence of cancer wherein hypomethylation of the specific nucleotide sequence or sequences indicates the presence of cancer cells in the subject. Nelson et al. teach that hypermethylation of the GSTP1 promoter is a characteristic of prostate cancer, however it does not teach that hypomethylation is characteristic of Wilm's tumour.

For at least the above reason, the present rejection of claim 23 should be withdrawn.

Respectfully submitted,

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